

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Johnson, Howard M.
Pontzer, Carol H.

(ii) TITLE OF INVENTION: Interferon Tau Compositions and
Methods of Use

(iii) NUMBER OF SEQUENCES: 44

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94306

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Filed herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/455,021
(B) FILING DATE: 31-MAY-1995

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/438,753
(B) FILING DATE: 10-MAY-1995

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/139,891
(B) FILING DATE: 19-OCT-1993

- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/847,741
 (B) FILING DATE: 09-MAR-1992
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/318,050
 (B) FILING DATE: 02-MAR-1989
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/969,890
 (B) FILING DATE: 30-OCT-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Dehlinger, Peter J.
 (B) REGISTRATION NUMBER: 28,006
 (C) REFERENCE/DOCKET NUMBER: 5600-0001.36
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 650-324-0880
 (B) TELEFAX: 650-324-0960
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Ovis aries
 (B) STRAIN: Domestic
 (D) DEVELOPMENTAL STAGE: Blastula (blastocyst)
 (F) TISSUE TYPE: Trophoctoderm

(G) CELL TYPE: Mononuclear trophoctoderm cells

(vii) IMMEDIATE SOURCE:

(B) CLONE: oTP-1a

(viii) POSITION IN GENOME:

(C) UNITS: bp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..516

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Ott, Troy L

Van Heeke, Gino

Johnson, Howard M

Bazer, Fuller W

(B) TITLE: Cloning and Expression in *Saccharomyces cerevisiae* of a Synthetic Gene for the Type I Trophoblast Interferon Ovine Trophoblast Protein-1: Purification and Antiviral Activity

(C) JOURNAL: J. Interferon Res.

(D) VOLUME: 11

(F) PAGES: 357-364

(G) DATE: 1991

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGC	TAC	CTG	TCG	CGA	AAA	CTG	ATG	CTG	GAC	GCT	CGA	GAA	AAT	TTA	AAA	48
Cys	Tyr	Leu	Ser	Arg	Lys	Leu	Met	Leu	Asp	Ala	Arg	Glu	Asn	Leu	Lys	
1				5				10				15				
CTG	CTG	GAC	CGT	ATG	AAT	CGA	TTG	TCT	CCG	CAC	AGC	TGC	CTG	CAA	GAC	96
Leu	Leu	Asp	Arg	Met	Asn	Arg	Leu	Ser	Pro	His	Ser	Cys	Leu	Gln	Asp	
			20				25					30				
CGG	AAA	GAC	TTC	GGT	CTG	CCG	CAG	GAA	ATG	GTT	GAA	GGT	GAC	CAA	CTG	144
Arg	Lys	Asp	Phe	Gly	Leu	Pro	Gln	Glu	Met	Val	Glu	Gly	Asp	Gln	Leu	
			35				40					45				

CAA AAA GAC CAA GCT TTC CCG GTA CTG TAT GAA ATG CTG CAG CAG TCT	192
Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser	
50 55 60	
TTC AAC CTG TTC TAC ACT GAA CAT TCT TCG GCC GCT TGG GAC ACT ACT	240
Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
65 70 75 80	
CTT CTA GAA CAA CTG TGC ACT GGT CTG CAA CAG CAA CTG GAC CAT CTG	288
Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Leu Asp His Leu	
85 90 95	
GAC ACT TGC CGT GGC CAG GTT ATG GGT GAA GAA GAC TCT GAA CTG GGT	336
Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly	
100 105 110	
AAC ATG GAT CCG ATC GTT ACT GTT AAA AAA TAT TTC CAG GGT ATC TAC	384
Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr	
115 120 125	
GAC TAC CTG CAG GAA AAA GGT TAC TCT GAC TGC GCT TGG GAA ATC GTA	432
Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
130 135 140	
CGC GTT GAA ATG ATG CCG GCC CTG ACT GTG TCG ACT ACT CTG CAA AAA	480
Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys	
145 150 155 160	
CGG TTA ACT AAA ATG GGT GGT GAC CTG AAT TCT CCG	516
Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro	
165 170	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of a mature
OvIFNtau protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
1 5 10 15
Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu
35 40 45
Gln Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
50 55 60
Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80
Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu
85 90 95
Asp Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly
100 105 110
Asn Met Asp Pro Ile Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr
115 120 125
Asp Tyr Leu Gln Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
130 135 140
Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr Leu Gln Lys
145 150 155 160
Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
165 170

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: synthetic nucleotide sequence encoding
 a mature human interferon-tau protein, HuIFNtau1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTGACTTGT CTCAAAACCA CGTTTGGTT GGTAGAAAGA ACTTAAGACT ACTAGACGAA	60
ATGAGACGTC TATCTCCACG CTTCTGTCTA CAAGACAGAA AGGACTTCGC TTGCGCTCAG	120
GAAATGGTIG AAGGTGGCCA ACTACAAGAA GCTCAAGCGA TATCTGTTTT GCACGAAATG	180
TTGCAACAAA GCTTCAACTT GTTCCACACC GAACACTCTT CGGCCGCTTG GGCACACCACC	240
TTGTTGGAAC AGCTCAGAAC CGGTTTGCAC CAACAATGG ACAACTTGA TGCAATGTTG	300
GGTCAAGTTA TGGGTGAAGA AGACTCTGCT CTCGGGAGAA CCGGTCCAAC GCTAGCTTTG	360
AAGAGATACT TCCAAGGTAT CCACGTTTAC TTGAAGGAAA AGGGTTACTC TGACTGTGCT	420
TGGGAAACCG TGCCTCTAGA AATCATGCGT AGCTTCTCTT CTTTGATCAG CTTGCAAGAA	480
AGATTACGTA TGATGGACGG TGACTTGTCT AGCCCA	516

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence for a mature
HuIFNtau protein, HuIFNtauL.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys	Asp	Leu	Ser	Gln	Asn	His	Val	Leu	Val	Gly	Arg	Lys	Asn	Leu	Arg
1				5					10					15	
Leu	Leu	Asp	Glu	Met	Arg	Arg	Leu	Ser	Pro	Arg	Phe	Cys	Leu	Gln	Asp
			20					25					30		
Arg	Lys	Asp	Phe	Ala	Leu	Pro	Gln	Glu	Met	Val	Glu	Gly	Gly	Gln	Leu
	35						40					45			
Gln	Glu	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Leu	Gln	Gln	Ser
	50					55					60				
Phe	Asn	Leu	Phe	His	Thr	Glu	His	Ser	Ser	Ala	Ala	Trp	Asp	Thr	Thr
65				70						75				80	
Leu	Leu	Glu	Gln	Leu	Arg	Thr	Gly	Leu	His	Gln	Gln	Leu	Asp	Asn	Leu
			85					90						95	
Asp	Ala	Cys	Leu	Gly	Gln	Val	Met	Gly	Glu	Glu	Asp	Ser	Ala	Leu	Gly
		100						105					110		
Arg	Thr	Gly	Pro	Thr	Leu	Ala	Leu	Lys	Arg	Tyr	Phe	Gln	Gly	Ile	His
	115						120					125			
Val	Tyr	Leu	Lys	Glu	Lys	Gly	Tyr	Ser	Asp	Cys	Ala	Trp	Glu	Thr	Val
	130					135						140			
Arg	Leu	Glu	Ile	Met	Arg	Ser	Phe	Ser	Ser	Leu	Ile	Ser	Leu	Gln	Glu
145				150						155				160	
Arg	Leu	Arg	Met	Met	Asp	Gly	Asp	Leu	Ser	Ser	Pro				
				165						170					

09746315.1424724

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 1-37
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys
5 10 15
Leu Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Gly
35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 34-64
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Asp Phe Gly Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu Gln
5 10 15

Lys Asp Gln Ala Phe Pro Val Leu Tyr Glu Met Leu Gln Gln Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 62-92
 of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Gln Ser Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp
 5 10 15

Asp Thr Thr Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln
 20 25 30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 90-122
 of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Gln Gln Leu Asp His Leu Asp Thr Cys Arg Gly Gln Val Met Gly
5 10 15

Glu Glu Asp Ser Glu Leu Gly Asn Met Asp Pro Ile Val Thr Val Lys
20 25 30

Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 119-150
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr Asp Tyr Leu Gln Glu Lys
5 10 15

Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: amino acid sequence of fragment 139-172
of SEQ ID NO:2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg Ala Leu Thr Val
5 10 15

Ser Thr Thr Leu Gln Lys Arg Leu Thr Lys Met Gly Gly Asp Leu Asn
20 25 30

Ser Pro

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau1 Human Interferon Tau coding
sequence with a leader sequence.

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC TAC
Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
1 5 10 15

48

GGC CCA GGA GGA TCC CTG GGT TGT GAC CTG TCT CAG AAC CAC GTG CTG	96
Gly Pro Gly Gly Ser Leu Gly Cys Asp Leu Ser Gln Asn His Val Leu	
20 25 30	
GTT GGC AGG AAG AAC CTC AGG CTC CTG GAC GAA ATG AGG AGA CTC TCC	144
Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser	
35 40 45	
CCT CGC TTT TGT CTG CAG GAC AGA AAA GAC TTC GCT TTA CCC CAG GAA	192
Pro Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu	
50 55 60	
ATG GTG GAG GGC GGC CAG CTC CAG GAG GCC CAG GCC ATC TCT GTG CTC	240
Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu	
65 70 75 80	
CAT GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA GAG CAC TCC	288
His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser	
85 90 95	
TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT GGA CTC	336
Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu	
100 105 110	
CAT CAG CAG CTG GAC AAC CTG GAT GCC TGC CTG GGG CAG GTG ATG GGA	384
His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly	
115 120 125	
GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG GCT CTG AAG	432
Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys	
130 135 140	
AGG TAC TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAC AGC	480
Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser	
145 150 155 160	
GAC TGC GCC TGG GAA ACC GTC AGA CTG GAA ATC ATG AGA TCC TTC TCT	528
Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser	
165 170 175	

TCA TTA ATC AGC TTG CAA GAA AGG TTA AGA ATG ATG GAT GGA GAC CTG 576
 Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu
 180 185 190

AGC TCA CCT TGA 588
 Ser Ser Pro
 195

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:11 (HuIFNtau1).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ala	Phe	Val	Leu	Ser	Leu	Leu	Met	Ala	Leu	Val	Leu	Val	Ser	Tyr
1					5				10					15	
Gly	Pro	Gly	Gly	Ser	Leu	Gly	Cys	Asp	Leu	Ser	Gln	Asn	His	Val	Leu
					20				25					30	
Val	Gly	Arg	Lys	Asn	Leu	Arg	Leu	Asp	Glu	Met	Arg	Arg	Leu	Ser	
					35				40					45	
Pro	Arg	Phe	Cys	Leu	Gln	Asp	Arg	Lys	Asp	Phe	Ala	Leu	Pro	Gln	Glu
					50				55					60	
Met	Val	Glu	Gly	Gly	Gln	Leu	Gln	Glu	Ala	Gln	Ala	Ile	Ser	Val	Leu
					65				70					75	
His	Glu	Met	Leu	Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Thr	Glu	His	Ser
					85				90					95	

Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu
100 105 110

His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly
115 120 125

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys
130 135 140

Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser
145 150 155 160

Asp Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser
165 170 175

Ser Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu
180 185 190

Ser Ser Pro
195

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: 25-mer synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTGTCTGCA GGACAGAAAA GACTT

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: 25-mer synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCTGAATTCT GACGATTTC CAGGC

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
1-37 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys	Asp	Leu	Ser	Gln	Asn	His	Val	Leu	Val	Gly	Arg	Lys	Asn	Leu	Arg
1					5				10					15	
Leu	Leu	Asp	Glu	Met	Arg	Arg	Leu	Ser	Pro	Arg	Phe	Cys	Leu	Gln	Asp
			20						25				30		
Arg	Lys	Asp	Phe	Ala											

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

[C] INDIVIDUAL ISOLATE: Amino acid sequence of fragment
34-64 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Lys	Asp	Phe	Ala	Leu	Pro	Gln	Glu	Met	Val	Glu	Gly	Gly	Gln	Leu	Gln
1				5					10					15	

Glu	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Leu	Gln	Gln	Ser
				20				25					30	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

[C] INDIVIDUAL ISOLATE: Amino acid sequence of fragment
62-92 of SEQ ID NO:4

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
119-150 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala	Leu	Lys	Arg	Tyr	Phe	Gln	Gly	Ile	His	Val	Tyr	Leu	Lys	Glu	Lys
1					5				10				15		
Gly	Tyr	Ser	Asp	Cys	Ala	Trp	Glu	Thr	Val	Arg	Leu	Glu	Ile	Met	Arg
				20				25					30		

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
139-172 of SEQ ID NO:4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Cys	Ala	Trp	Glu	Thr	Val	Arg	Leu	Glu	Ile	Met	Arg	Ser	Phe	Ser	Ser
1				5				10					15		
Leu	Ile	Ser	Leu	Gln	Glu	Arg	Leu	Arg	Met	Met	Asp	Gly	Asp	Leu	Ser
				20				25					30		

Ser Pro

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau6

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

C	CAG	GAG	ATG	GTG	GAG	GGC	GGC	CAG	CTC	CAG	GAG	GCC	CAG	GCC	ATC	46
	Gln	Glu	Met	Val	Glu	Gly	Gly	Gln	Leu	Gln	Glu	Ala	Gln	Ala	Ile	
	1				5				10					15		
TCT	GTG	CTC	CAC	AAG	ATG	CTC	CAG	CAG	AGC	TTC	AAC	CTC	TTC	CAC	ACA	94
Ser	Val	Leu	His	Lys	Met	Leu	Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Thr	
				20					25					30		
GAG	CGC	TCC	TCT	GCT	GCC	TGG	GAC	ACC	ACC	CTC	CTG	GAG	CAG	CTC	CGC	142
Glu	Arg	Ser	Ser	Ala	Ala	Trp	Asp	Thr	Thr	Leu	Leu	Glu	Gln	Leu	Arg	
				35				40						45		
ACT	GGA	CTC	CAT	CAG	CAG	CTG	GAT	GAC	CTG	GAC	GCC	TGC	CTG	GGG	CAG	190
Thr	Gly	Leu	His	Gln	Gln	Leu	Asp	Asp	Leu	Asp	Ala	Cys	Leu	Gly	Gln	
				50				55						60		
GTG	ACG	GGA	GAG	GAA	GAC	TCT	GCC	CTG	GGA	AGG	ACG	GGC	CCC	ACC	CTG	238
Val	Thr	Gly	Glu	Glu	Asp	Ser	Ala	Leu	Gly	Arg	Thr	Gly	Pro	Thr	Leu	
				65				70						75		

GCC GTG AAG AGC TAC TTC CAG GGC ATC CAT ATC TAC CTG CAA GAG AAG 286
 Ala Val Lys Ser Tyr Phe Gln Gly Ile His Ile Tyr Leu Gln Glu Lys
 80 85 90 95

GGA TAC AGC GAC T 299
 Gly Tyr Ser Asp

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:21 (HuIFNtau6).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser
 1 5 10 15
 Val Leu His Lys Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu
 20 25 30
 Arg Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr
 35 40 45
 Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val
 50 55 60
 Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala
 65 70 75 80
 Val Lys Ser Tyr Phe Gln Gly Ile His Ile Tyr Leu Gln Glu Lys Gly
 85 90 95
 Tyr Ser Asp

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau7

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

C	CAG	GAG	ATG	GTG	GAG	GTC	AGC	CAG	TTC	CAG	GAG	GCC	CAG	GCC	ATT	46
	Gln	Glu	Met	Val	Glu	Val	Ser	Gln	Phe	Gln	Glu	Ala	Gln	Ala	Ile	
	1				5					10				15		
TCT	GTG	CTC	CAT	GAG	ATG	CTC	CAG	CAG	AGC	TTC	AAC	CTC	TTC	CAC	AAA	94
	Ser	Val	Leu	His	Glu	Met	Leu	Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Lys
					20					25				30		
GAG	CGC	TCC	TCT	GCT	GCC	TGG	GAC	ACT	ACC	CTC	CTG	GAG	CAG	CTC	CTC	142
	Glu	Arg	Ser	Ser	Ala	Ala	Trp	Asp	Thr	Thr	Leu	Leu	Glu	Gln	Leu	Leu
					35					40				45		
ACT	GGA	CTC	CAT	CAG	CAG	CTG	GAT	GAC	CTG	GAT	GCC	TGT	CTG	GGG	CAG	190
	Thr	Gly	Leu	His	Gln	Gln	Leu	Asp	Asp	Leu	Asp	Ala	Cys	Leu	Gly	Gln
					50					55				60		

TTG ACT GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG 238
 Leu Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu
 65 70 75

GCC GTG AAG AGC TAC TTC CAG GGC ATC CAT GTC TAC CTG CAA GAG AAG 286
 Ala Val Lys Ser Tyr Phe Gln Gly Ile His Val Tyr Leu Gln Glu Lys
 80 85 90 95

GG 288

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:23 (HuIFNtau7).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gln Glu Met Val Glu Val Ser Gln Phe Gln Glu Ala Gln Ala Ile Ser
 1 5 10 15

Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Lys Glu
 20 25 30

Arg Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Leu Thr
 35 40 45

Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Leu
 50 55 60

Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala
 65 70 75 80

Val Lys Ser Tyr Phe Gln Gly Ile His Val Tyr Leu Gln Glu Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 307 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau4

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

C	CAG	GAG	ATG	GTG	GAG	GGT	GGC	CAG	CTC	CAG	GAG	GCC	CAG	GCC	ATC	46
	Gln	Glu	Met	Val	Glu	Gly	Gly	Gln	Leu	Gln	Glu	Ala	Gln	Ala	Ile	
	1				5					10					15	
TCT	GTG	CTC	CAC	GAG	ATG	CTC	CAG	CAG	AGC	TTC	AAC	CTC	TTC	CAC	ACA	94
Ser	Val	Leu	His	Glu	Met	Leu	Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Thr	
					20					25					30	
GAG	CAC	TCC	TCT	GCT	GCC	TGG	GAC	ACC	ACC	CTC	CTG	GAG	CAG	CTC	CGC	142
Glu	His	Ser	Ser	Ala	Ala	Trp	Asp	Thr	Thr	Leu	Leu	Glu	Gln	Leu	Arg	
					35					40					45	

ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG GAT GCC TGC CTG GGG CAG 190
 Thr Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln
 50 55 60

GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG 238
 Val Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu
 65 70 75

GCC ATG AAG ACG TAT TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG 286
 Ala Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys
 80 85 90 95

GGA TAT AGT GAC TGC GCC TGG 307
 Gly Tyr Ser Asp Cys Ala Trp
 100

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:25 (HuIFNtau4).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser
 1 5 10 15

Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu
 20 25 30

His Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr
 35 40 45

Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val
50 55 60

Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala
65 70 75 80

Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly
85 90 95

Tyr Ser Asp Cys Ala Trp
100

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau5

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

C CAG GAG ATG GTG GAG GGT GGC CAG CTC CAG GAG GCC CAG GCC ATC 46
Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile
1 5 10 15

TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA 94
 Ser Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr
 20 25 30

GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC 142
 Glu His Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg
 35 40 45

ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG GAT GCC TGC CTG GGG CAG 190
 Thr Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln
 50 55 60

GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG 238
 Val Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu
 65 70 75

GCC ATG AAG ACG TAT TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG 286
 Ala Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys
 80 85 90 95

GGA TAT AG 294
 Gly Tyr

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:27 (HuIFNtau5).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Gln Glu Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser
 1 5 10 15

Val Leu His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu
20 25 30

His Ser Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr
35 40 45

Gly Leu His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val
50 55 60

Thr Gly Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala
65 70 75 80

Met Lys Thr Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly
85 90 95

Tyr

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau2

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGG AAG AAC CTC AGG CTC
Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg Leu
1 5 10 15

48

CTG GAC CAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG CAG GAC AGA	96
Leu Asp Gln Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp Arg	
20 25 30	
AAA GAC TTC GCT TTA CCC TAG GAA ATG GTG GAG GGC GGC CAG CTC CAG	144
Lys Asp Phe Ala Leu Pro Glu Met Val Glu Gly Gly Gln Leu Gln	
35 40 45	
GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC TTC	192
Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser Phe	
50 55 60	
AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC	240
Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr Leu	
65 70 75 80	
CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAC AAC CTG GAT	288
Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu Asp	
85 90 95	
GCC TGC CTG GGG CAG GTG ATG GGA GAG GAA GAC TCT GCC CTG GGA AGG	336
Ala Cys Leu Gly Gln Val Met Gly Glu Asp Ser Ala Leu Gly Arg	
100 105 110	
ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG GGC ATC CAT GTC	384
Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His Val	
115 120 125	
TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC AGA	432
Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val Arg	
130 135 140	
GTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA AGG	480
Val Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu Arg	
145 150 155 160	
TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA	516
Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro	
165 170	

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 115-117
 (D) OTHER INFORMATION: /note= "to allow expression of the
 encoded protein this site can be modified
 to encode an amino acid, e.g., Gln"

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:29 (HuIFNtau2).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp	Leu	Ser	Gln	Asn	His	Val	Leu	Val	Gly	Arg	Lys	Asn	Leu	Arg	Leu
1				5					10					15	
Leu	Asp	Gln	Met	Arg	Arg	Leu	Ser	Pro	Arg	Phe	Cys	Leu	Gln	Asp	Arg
			20						25					30	
Lys	Asp	Phe	Ala	Leu	Pro	Xaa	Glu	Met	Val	Glu	Gly	Gly	Gln	Leu	Gln
			35						40					45	
Glu	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Leu	Gln	Gln	Ser	Phe
			50						55					60	
Asn	Leu	Phe	His	Thr	Glu	His	Ser	Ser	Ala	Ala	Trp	Asp	Thr	Thr	Leu
			65						70					75	
Leu	Glu	Gln	Leu	Arg	Thr	Gly	Leu	His	Gln	Gln	Leu	Asp	Asn	Leu	Asp
									85					90	
Ala	Cys	Leu	Gly	Gln	Val	Met	Gly	Glu	Glu	Asp	Ser	Ala	Leu	Gly	Arg
														110	

Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His Val
 115 120 125

Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val Arg
 130 135 140

Val Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu Arg
 145 150 155 160

Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
 165 170

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 39
- (D) OTHER INFORMATION: /note= "where Xaa a selected amino acid,
 for example, Gln"

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: HuIFNtau3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC TAC	48
Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr	
1 5 10 15	
GGC CCG GGA GGA TCC CTG CGG TGT GAC CTG TCT CAG AAC CAC GTG CTG	96
Gly Pro Gly Gly Ser Leu Arg Cys Asp Leu Ser Gln Asn His Val Leu	
20 25 30	
GTT GGC AGC CAG AAC CTC AGG CTC CTG GGC CAA ATG AGG AGA CTC TCC	144
Val Gly Ser Gln Asn Leu Arg Leu Leu Gly Gln Met Arg Arg Leu Ser	
35 40 45	
CTT CGC TTC TGT CTG CAG GAC AGA AAA GAC TTC GCT TTC CCC CAG GAG	192
Leu Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Phe Pro Gln Glu	
50 55 60	
ATG GTG GAG GGT GGC CAG CTC CAG GAG GCC CAG GCC ATC TCT GTG CTC	240
Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu	
65 70 75 80	
CAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC CAC ACA GAG CAC TCC	288
His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser	
85 90 95	
TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT GGA CTC	336
Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Gln Leu Arg Thr Gly Leu	
100 105 110	
CAT CAG CAG CTG GAT GAC CTG GAT GCC TGC CTG GGG CAG GTG ACG GGA	384
His Gln Gln Leu Asp Asp Leu Ala Cys Leu Gly Gln Val Thr Gly	
115 120 125	
GAG GAA GAC TCT GCC CTG GGA AGA ACG GGC CCC ACC CTG GCC ATG AAG	432
Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Met Lys	
130 135 140	
AGG TAT TTC CAG GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAT AGT	480
Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser	
145 150 155 160	

GAC TGC GCC TGG GAA ATT GTC AGA CTG GAA ATC ATG AGA TCC TTG TCT 528
 Asp Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg Ser Leu Ser
 165 170 175

TCA TCA ACC AGC TTG CAC AAA AGG TTA AGA ATG ATG GAT GGA GAC CTG 576
 Ser Ser Thr Ser Leu His Lys Arg Leu Arg Met Met Asp Gly Asp Leu
 180 185 190

AGC TCA CCT TGA 588
 Ser Ser Pro
 195

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: predicted amino acid coding sequence
 of SEQ ID NO:31 (HuIFNtau3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
 1 5 10 15

Gly Pro Gly Gly Ser Leu Arg Cys Asp Leu Ser Gln Asn His Val Leu
 20 25 30

Val Gly Ser Gln Asn Leu Arg Leu Leu Gly Gln Met Arg Arg Leu Ser
 35 40 45

Leu Arg Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Phe Pro Gln Glu
 50 55 60

Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu
 65 70 75 80

His	Glu	Met	Leu	Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Thr	Glu	His	Ser
						85								90	95
Ser	Ala	Ala	Trp	Asp	Thr	Thr	Leu	Leu	Glu	Gln	Leu	Arg	Thr	Gly	Leu
			100						105					110	
His	Gln	Gln	Leu	Asp	Asp	Leu	Asp	Ala	Cys	Leu	Gly	Gln	Val	Thr	Gly
			115					120					125		
Glu	Glu	Asp	Ser	Ala	Leu	Gly	Arg	Thr	Gly	Pro	Thr	Leu	Ala	Met	Lys
		130					135					140			
Arg	Tyr	Phe	Gln	Gly	Ile	His	Val	Tyr	Leu	Lys	Glu	Lys	Gly	Tyr	Ser
145					150					155					160
Asp	Cys	Ala	Trp	Glu	Ile	Val	Arg	Leu	Glu	Ile	Met	Arg	Ser	Leu	Ser
				165					170					175	
Ser	Ser	Thr	Ser	Leu	His	Lys	Arg	Leu	Arg	Met	Met	Asp	Gly	Asp	Leu
				180					185					190	
Ser	Ser	Pro													
			195												

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau3, mature no leader sequence

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGC CAG AAC CTC AGG	48
Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg	
1 5 10 15	
CTC CTG GGC CAA ATG AGG AGA CTC TCC CTT CGC TTC TGT CTG CAG GAC	96
Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp	
20 25 30	
AGA AAA GAC TTC GCT TTC CCC CAG GAG ATG GTG GAG GGT GGC CAG CTC	144
Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu	
35 40 45	
CAG GAG GCC CAG GCC ATC TCT GTG CTC CAC GAG ATG CTC CAG CAG AGC	192
Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser	
50 55 60	
TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC	240
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
65 70 75 80	
CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAT GAC CTG	288
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu	
85 90 95	
GAT GCC TGC CTG GGG CAG GTG ACG GGA GAG GAA GAC TCT GCC CTG GGA	336
Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly	
100 105 110	
AGA ACG GGC CCC ACC CTG GCC ATG AAG AGG TAT TTC CAG GGC ATC CAT	384
Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His	
115 120 125	
GTC TAC CTG AAA GAG AAG GGA TAT AGT GAC TGC GCC TGG GAA ATT GTC	432
Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val	
130 135 140	

AGA CTG GAA ATC ATG AGA TCC TTG TCT TCA TCA ACC AGC TTG CAC AAA 480
Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys
145 150 155 160

AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT TG 518
Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
165 170

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
1 5 10 15
Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp
20 25 30
Arg Lys Asp Phe Ala Phe Pro Gln Glu Met Val Glu Gly Gly Gln Leu
35 40 45
Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
50 55 60
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asp Leu
85 90 95
Asp Ala Cys Leu Gly Gln Val Thr Gly Glu Glu Asp Ser Ala Leu Gly
100 105 110

Arg Thr Gly Pro Thr Leu Ala Met Lys Arg Tyr Phe Gln Gly Ile His
115 120 125

Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val
130 135 140

Arg Leu Glu Ile Met Arg Ser Leu Ser Ser Ser Thr Ser Leu His Lys
145 150 155 160

Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
165 170

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
1-37 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Ser Gln Asn Leu Arg
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Ser Leu Arg Phe Cys Leu Gln Asp
20 25 30

Arg Lys Asp Phe Ala
35

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
34-64 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys	Asp	Phe	Ala	Phe	Pro	Gln	Glu	Met	Val	Glu	Gly	Gly	Gln	Leu	Gln
1					5				10					15	
Glu	Ala	Gln	Ala	Ile	Ser	Val	Leu	His	Glu	Met	Leu	Gln	Gln	Ser	
				20				25						30	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
62-92 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln	Gln	Ser	Phe	Asn	Leu	Phe	His	Thr	Glu	His	Ser	Ser	Ala	Ala	Trp
1					5				10					15	
Asp	Thr	Thr	Leu	Leu	Glu	Gln	Leu	Arg	Thr	Gly	Leu	His	Gln	Gln	
				20				25						30	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
90-122 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

His Gln Gln Leu Asp Asp Leu Asp Ala Cys Leu Gly Gln Val Thr Gly
1 5 10 15

Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Thr Leu Ala Met Lys
20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
119-150 of SEQ ID NO:33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala Met Lys Arg Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys
1 5 10 15

Gly Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg
20 25 30

[illegible]

(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
139-172 of SEQ ID NO:33

Cys Ala Trp Glu Ile Val Arg Leu Glu Ile Met Arg Ser Leu Ser Ser
1 5 10 15
Ser Thr Ser Leu His Lys Arg Leu Arg Met Met Asp Gly Asp Leu Ser
20 25 30
Ser Pro

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
1-23 of SEQ ID NO:32

146

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
 1 5 10 15
 Gly Pro Gly Gly Ser Leu Arg
 20

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Amino acid sequence of fragment
 1-23 of SEQ ID NO:11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr
 1 5 10 15
 Gly Pro Gly Gly Ser Leu Gly
 20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HuIFNtau1 genomic-derived
DNA coding sequence, without leader seq.

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC AGG AAG AAC CTC AGG	48
Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg	
1 5 10 15	
CTC CTG GAC GAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG CAG GAC	96
Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp	
20 25 30	
AGA AAA GAC TTC GCT TTA CCC CAG GAA ATG GTG GAG GGC GGC CAG CTC	144
Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu	
35 40 45	
CAG GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC	192
Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser	
50 55 60	
TTC AAC CTC TTC CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC	240
Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr	
65 70 75 80	
CTC CTG GAG CAG CTC CGC ACT GGA CTC CAT CAG CAG CTG GAC AAC CTG	288
Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu	
85 90 95	
GAT GCC TGC CTG GGG CAG GTG ATG GGA GAG GAA GAC TCT GCC CTG GGA	336
Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu Gly	
100 105 110	
AGG ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG GGC ATC CAT	384
Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile His	
115 120 125	

GTC TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC 432
Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr Val
130 135 140

AGA CTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA 480
Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln Glu
145 150 155 160

AGG TTA AGA ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA 519
Arg Leu Arg Met Met Asp Gly Asp Leu Ser Ser Pro
165 170

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Cys Asp Leu Ser Gln Asn His Val Leu Val Gly Arg Lys Asn Leu Arg
1 5 10 15

Leu Leu Asp Glu Met Arg Arg Leu Ser Pro Arg Phe Cys Leu Gln Asp
20 25 30

Arg Lys Asp Phe Ala Leu Pro Gln Glu Met Val Glu Gly Gly Gln Leu
35 40 45

Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln Ser
50 55 60

Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr Thr
65 70 75 80

Leu Leu Glu Gln Leu Arg Thr Gly Leu His Gln Gln Leu Asp Asn Leu
85 90 95

Asp	Ala	Cys	Leu	Gly	Gln	Val	Met	Gly	Glu	Glu	Asp	Ser	Ala	Leu	Gly
			100					105						110	
Arg	Thr	Gly	Pro	Thr	Leu	Ala	Leu	Lys	Arg	Tyr	Phe	Gln	Gly	Ile	His
		115						120					125		
Val	Tyr	Leu	Lys	Glu	Lys	Gly	Tyr	Ser	Asp	Cys	Ala	Trp	Glu	Thr	Val
		130					135						140		
Arg	Leu	Glu	Ile	Met	Arg	Ser	Phe	Ser	Ser	Leu	Ile	Ser	Leu	Gln	Glu
		145				150					155				160
Arg	Leu	Arg	Met	Met	Asp	Gly	Asp	Leu	Ser	Ser	Pro				
					165						170				